NTNU

Kunnskap for en bedre verden

Master’s theses proposals

Department of Biotechnology

Department of Biology

This document contains proposed projects relevant for students at MSc Biotechnology (2- and 5-year study), MSc Aquatic Food Production, the 2-and 5 year MSc Chemical Engineering and Biotechnology (MKIJ/MTKJ) and Nanotechnology (MTNANO) (sivilingeniørstudiet).

The different proposals might have different credits. This relates to the proposed theses being planned for different study programmes: the MSc Biotechnology (60 credits), MSc Aquatic Food Production (30 credits) or MSc Chemical Engineering and Biotechnology (30 credits). Some proposals may also be relevant as specialization project (15 credits)

Please contact supervisor directly if you have any questions regarding theses’ proposals.

Academic year 2016/17

Date: 09.03.2016 (update 2)

Contents

Department of Biotechnology

Hovedveileder: *Main supervisor:*	Finn L. Aachmann
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Biveileder/-e: *Co-supervisor/-s:*	Gaston Courtade
Arbeidstittel på oppgaven/ *Preliminary title:*	**Development of chitin-based sorbents for protein purification**

Kort beskrivelse av oppgaven / *Short description of the project*:
The focus of this project will be to design and construct chitin-based materials for the extraction and purification of proteins from complex biological mixtures.

Bakgrunn og mål / *Background and Objectives:*
The production of proteins is a high-value industry with applications in all branches of biotechnology. A key step of the protein-production process is to achieve a high degree of purity of the protein products. Affinity chromatography is a powerful tool for the purification of specific proteins from a complex biological mixture, such as a fermenter. Chitin is a polysaccharide that is a good candidate for use in affinity chromatography because it selectively adsorbs proteins that bind chitin. In fact, chitin resins are already employed in affinity chromatography columns. However, the use of columns requires some degree of sample preparation and filtration. The aim of this project is to develop chitin-based materials that can be used for direct extraction of proteins from biological mixtures. Such materials would provide a rapid alternative method to extract and purify target proteins at different stages of a process without the need for sample preparation.

Eksperimentelt / *Experimental methods:*

- Development of methods for the production of chitin fibers.
- Characterization of chitin fibers (strength, swelling, protein adsorption).
- Design of a protocol for the use of chitin fibers in protein purification applications.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MTNANO
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng 60 credits / 30 credits

Hovedveileder: *Main supervisor:*	Finn L. Aachmann
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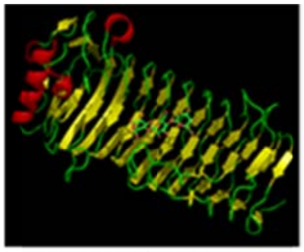
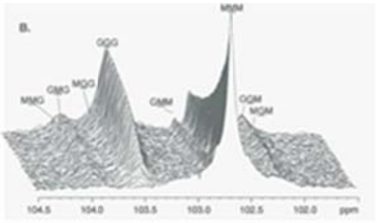
Biveileder/-e: *Co-supervisor/-s:*	Marit Sletmoen og/eller Anne Tøndervik (Sintef)
Arbeidstittel på oppgaven/ *Preliminary title:*	**Purification and characterization of design mannuronan-c-5 epimerases**

Kort beskrivelse av oppgaven / *Short description of the project*:
The focus of this project will be to study the interaction of alginate C-5 epimerases with substrate, and its product profile using biophysical techniques. The specific content of project may be adapted to the candidate's preferences.

Bakgrunn og mål / *Background and Objectives:*
Azotobacter vinelandii is a soil bacteria, which are able to produce alginate, a polysaccharide. Alginate consists of mannuronic acid (M) and guluronic acid (G), and the properties of the polymer are, among other things, dependent on the distribution of these units. *A. vinelandii* synthesises alginate by first making polymannuronic acid (poly-M), of which some M-units are converted to G-units. This reaction is catalyzed by enzymes called epimerases, and *A. vinelandii* produce seven enzymes of this kind; AlgE1 to AlgE7. Poly-M can be epimerized in vitro and the various epimerases are shown to give different G-contents and different distributions of G-unites in the alginate that is produced


A-module of AlgE4

Certain alginates have turned out to be bioactive, and are therefore interesting with regards to medical applications. Researchers at NTNU/Sintef are trying to find new enzymes that can create alginates with tailored properties for these kinds of applications. This project will be about characterization of alginate epimerases. This involves protein production and purification of the enzymes. Characterization of the properties of the enzymes with regard to epimerization of poly-M. Gelling properties of the generated alginates and characterization.



Epimerase activity profile by NMR

Eksperimentelt / *Experimental methods:*

- Production and purification of the alginate epimerases.
- Characterization of the enzymes with regard to activity, substrate specificity and reaction pattern. Relevant methods for the characterization are Isothermal titration calorimetry (ITC), atomic force microscopy (AFM), Ion chromatography system (ICS), NMR and Time-resolved NMR.
- Characterization of epimerized alginates with regard to gelling properties, relevant for their biomedical applications.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MTNANO
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng 60 credits / 30 credits

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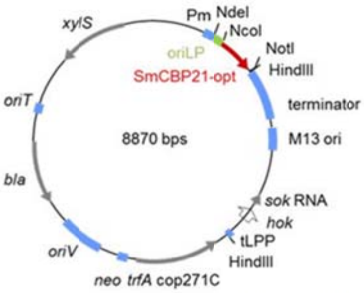
Biveileder/-e: *Co-supervisor/-s:*	Trygve Brautaset
Arbeidstittel på oppgaven/ *Preliminary title:*	**New heterologous protein expression system for isotope labeled proteins**

Kort beskrivelse av oppgaven / *Short description of the project*:
This project will focus on the further development of a new set of expression vectors for production of isotope labeled protein (for NMR applications) based on the *Pm*/XylS promoter system. The specific content of the project may be adapted to the candidate's preferences.

Bakgrunn og mål / *Background and Objectives:*



Vector map of LPMO Expression cassette

A common bottleneck in heterologous protein expression of isotope labelled protein in bacteria is the promoter system used. These promoter systems are mainly based on the carbohydrate metabolism of the cell, like the *Lac* and *ara—BAD* operons. This poses a problem when growing cells in a minimal medium with glucose as the sole carbon source, which results in poor regulation of the promoter system and low expression of the target protein.

A solution to the problem is to use a promoter system that is not influenced by the carbohydrate metabolism of the cell. The group of Prof. Svein Valla at our department has developed an expression system based on the *Pm*/XylS promoter system, which uses benzoate derivatives as inducers of the protein expression. Recently, we have published a work where *Pm*/XylS promoter system was used for the expression of an isotope labeled LPMO (lytic polysaccharide monooxygenase).

Aim of this project is to construct a new set of expression vectors for production of isotope labeled protein where expression level of the target protein is independent of media composition. The developed expression system will offer a large potential within structural biology and for protein expression in general.

Eksperimentelt / *Experimental methods:*

- *State-of-the-art* molecular genetics.
- Characterization of the of the expression system.
- Production and purification of the target protein.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MTNANO
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng 60 credits / 30 credits

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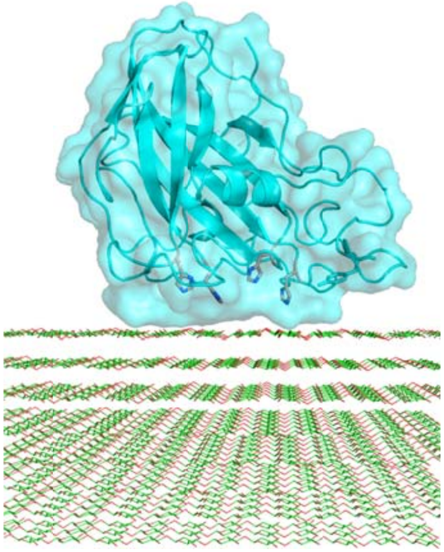
Biveileder/-e: *Co-supervisor/-s:*	Gaston Courtade
Arbeidstittel på oppgaven/ *Preliminary title:*	**Characterization of novel proteins for biorefinery applications**

Kort beskrivelse av oppgaven / *Short description of the project*:
The focus of this project will be to study new carbohydrate active enzymes by using biophysical techniques such as NMR spectroscopy. The specific content of project may be adapted to the candidate's preferences.

Bakgrunn og mål / *Background and Objectives:*
Biorefineries where biomass from marine and forestry resources are converted to monosaccharides are a cornerstone of bioeconomy. These monosaccharides can be used to produce bioethanol and value-added products. However, the inefficient hydrolysis of insoluble biomass (chitin and cellulose) is a bottleneck in the biorefining process. A way to overcome this obstacle is through a new family of enzymes - lytic polysaccharide monooxygenases (LPMOs) – that enhance the biomass degradation process by the oxidative cleavage of glycosidic bonds in chitin and cellulose. Since 2010, we have studied LPMOs in cooperation with NMBU, and we are interested in gaining a better understanding of the function and mode of action of LPMOs.



Eksperimentelt / *Experimental methods:*

- Recombinant protein production and purification.
- Acquisition of multidimensional NMR spectra and assignment of the protein backbone and side-chains.
- Protein structure determination.
- Dynamics studies with NMR spectroscopy and other techniques such as circular dichroism (CD).
- Measurements of interactions between LPMOs and other substrates/proteins.

Passer for (angi studieretning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MTNANO
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng 60 credits / 30 credits

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Please feel free to stop by my office. If you are interested in these general topics, but have a different problem in mind – let's talk!

Most of these projects can be adjusted to fit a 60sp or 15+30sp profile.

1. Biological network analysis

Network analysis has been central to uncovering important principles of interactome organization. Gene expression correlation networks consist of genes that showing strong similarities or dissimilarities in their expression patterns, making it possible to identify important gene clusters associated with a given phenotype or biological function.

a. Gene expression and protein interaction networks in *Arabidopsis thaliana* during stress conditions

Gen uttrykks- og protein interaksjonsnettverk i *Arabidopsis thaliana* under stress betingelser

In this project, the candidate will combine *Arabidopsis* mRNA expression data with its known protein interaction network. This project is in collaboration with Prof. Bones' group (IBI), which has generated transcription data on multiple conditions in *Arabidopsis*. The goal is to identify genes and gene clusters that change behavior during stress conditions, which may lead to the uncovering of functional pathways.

b. Comparative study of gene expression networks in *Synechocystis sp. PCC6803*

Sammenligning av gen-uttrykksnettverk i *Synechocystis sp. PCC6803*

In this project, the candidate will use a recently developed network approach (Voigt, Nowick & Almaas) to study evolution and conservation of gene expression correlations. The candidate will use the comprehensive database cyanoExpress, which contains gene expression data from 177 distinct genetic and environmental perturbation experiments for the cyanobacterium Synechocystis sp. PCC6803. Synechocystis is an important model organism for developing our understanding of photosynthesis, and the research focus will be on using network analysis methodology to study photosynthetic function. Co-mentor: Prof. Martin Hohmann-Marriott.

c. Comparative study of gene expression networks in *Homo sapiens*

Sammenligning av gen-uttryksnettverk i *Homo sapiens*

The ability to understand consequences of genetic variation among humans is a significant challenge in biology. The goal of this project is to use a recently developed network approach (Voigt, Nowick & Almaas) to study the variation of *gene co-expression patterns* in a recent high-quality gene-expression data set, GTEx (http://www.gtexportal.org/). The candidate will further develop the approach as well as applying it to GTEx data using a variety of human tissue types.

2. Metabolic Engineering

Flux Balance Analysis (FBA) is the central approach in modeling genome-scale metabolism, with its capability for predicting metabolic phenotypes and identifying possible approaches for engineering cellular behavior. A genome-scale model may be generated within 48 hours, and the COBRA toolbox in MatLab or for the programming language Python will be used to analyze the models.

a. Computational modeling of two-species microbial consortium

Modellering av mikrobielt samfunn bestående av to organismer

Using the "Computation Of Microbial Ecosystems in Time and Space" (COMETS)[1] computational framework for simulating microbial metabolism using FBA in a spatial structure, the aim of this project is to evaluate the effect of different competitive strategies between two chosen microbes.

b. Analysis of genotype-phenotype networks constructed from FBA modeling

Analyse av genotype-fenotype nettverk fra FBA modellering

Using the FBA approach together with an in-house compendium of possible metabolic models, the aim of this project is to generate genotype-phenotype mappings for a large set of metabolic models and analyze the properties of these networks using complex network approaches.

3. Antibiotic resistance modeling

The spread of antibiotic resistance in pathogens is becoming a severe threat to modern medicine. While the level of antibiotics use in Norway is comparatively low to other parts of the world, widespread travel patterns are sure to bring resistant strains to Norway even if resistance is not developed locally.

a. Computational modeling of antibiotic resistance spreading through horizontal gene transfer in bacterial populations

Modellering av spredning av antibiotikaresistens via horizontal gene utveksling i bakteripopulasjoner

The first part of this project consists of a literature survey of methods for computational modeling of antibiotic resistance spreading in bacterial populations, as well as mechanisms for known modes of horizontal gene transfer. The second part is to develop a model that will be solved computationally.

b. Computational modeling of evolution of antibiotic resistance in a bacterial species

Modellering av antibiotika resistens evolusjon i en bakterie

The first part of this project consists of a literature survey of methods for computational modeling of antibiotic resistance evolution in bacterial species, as well as mechanisms for resistance evolution. The second part is to develop a model that will be solved computationally.

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[1] http://www.bu.edu/segrelab/comets/

Master thesis in Biotechnology, 15, 30, 60 sp

Understanding the mucosal barrier: Bacteria-mucus interactions

Goal

In this interdisciplinary project, involving microbiology, rheology, and advanced high resolution microscopy, the aim is to elucidate how bacteria influence on the mechanical properties and the barrier function of mucus.

Background

Mucosal tissue, covering the body cavities of animals and the skin of fishes, constitutes a major barrier against microbes and other agents in the external environment. This barrier is permeable but selective, allowing the absorption of nutrients, electrolytes, and water, but preventing the penetration of pathogens, toxins, and antigens. It consists of a single layered sheet of epithelial cells covered with mucus. The mucus is continuously secreted and transported away from the epithelial cell layer, so that entrapped microbes or other agents are removed together with the mucus. Mucin glycoproteins are the major constituent of the mucus, and are responsible for the viscous properties. The mucus is colonized by resident microbiota, and this microbiota contributes to the barrier function and also influences on the mechanical properties of the mucus. However, the specific molecular mechanisms for interactions between bacteria and mucus and the implications for the barrier function are poorly understood.

In this project, we will take advantage of the expertise existing within several research groups at the Department of Biotechnology, to study mucus-bacteria interactions at a basic, molecular level. In particular, we will apply rheology, microscopy as well as microbiological approaches to examine consequences on barrier function and mechanical properties after exposure of mucus to various bacterial strains and communities. The focus will be on mucus from salmon skin, since this mucosal barrier is particularly important for fish health. Mucus with distinct properties, sampled for example from healthy individuals and from individuals exposed to sea lice, will be investigated.

Work description

The final design of the master projects will be determined by the supervisors together with the master students. Up to three master students can be involved in the project.

Relevant methods are:

- Cultivation of strains and selection for microbial communities with distinct properties
- Deep-sequencing approaches for taxonomic analysis of microbial communities associated with the salmon mucus
- Use of rheology and sensitive force probes to determine the viscoelastic properties of the mucus layer and how this changes after introduction of the microbial communities.
- Use of sensitive force probes to study the interaction between bacteria and mucus layer
- Characterisation of the mucosal barrier, including diffusion abilities of molecules through the barrier, using laser scanning fluorescence microscopy.

Supervisors: Catherine Taylor Nordgård (catherine.t.nordgard@ntnu.no), Marit Sletmoen (marit.sletmoen@ntnu.no), Torunn Forberg (torunn.forberg@ntnu.no), and Ingrid Bakke (ingrid.bakke@ntnu.no)

Master thesis in Biotechnology, 15, 30, 60 sp

Gut microbiota of salmon in recirculating aquaculture systems with different solids removal and loading

Goal

The objective of this master thesis is to investigate the development of the gut microbiota of salmon in recirculating aquaculture systems (RAS) at different operational conditions, and compare to the gut microbiota of fishes reared in a flow through system.

Background

This master thesis will be part of the SINTEF EU COFASP project RAS-ORGMAT, and the master student will work together with the project researchers and other master and PhD students. A brand new experimental rig built at NTNU SeaLab will be used in the experiment. The project aim to optimize removal of organic matter in land based aquaculture recirculation systems (RAS) to increase water/feed efficiency by reducing waste products and effecting carrying capacity of bacteria, lower the production cost by intensification, lower the environmental impact by separating and treating the organic matter from the water. We see rapid, gentle and efficient removal of particulate organic matter as the key to improve the production and product quality of fish produced in RAS. If the organic matter remains in the water, heterotrophic bacterial degradation significantly contributes to the consummation of oxygen and the production of CO_2 and other compounds. The supply of organic matter is the determining factor for the amount of bacteria that can be sustained in the RAS over time. Organic matter reduces the efficiency of both UV and ozone disinfection, contribute to color and stimulate bacteria producing off-flavor compounds, reducing the value of fish. In this project we will develop what we believe will the most optimal solution and combinations of technology to remove particles/organic matter and sense dissolved CO_2. Multiple drains with optimized geometry and hydraulics will be designed for early particles collection and to be used in combination with advanced membrane filtration technologies. A close collaboration with fish-producing companies will safeguard that the research and development will be applicable for commercial aquaculture use.

Work description

The project will involve an experiment with smolt in two different RAS configurations and one flow through system. The composition of the microbial communities in fish gut and skin will be studied by a 16S rDNA amplicon based strategy (DNA extraction, PCR, DGGE, DNA sequencing).

Supervisors: Kari Attramadal Kari Attramadal (kari.attramadal@ntnu.no), Olav Vadstein (olav.vadstein@ntnu.no), and Ingrid Bakke (ingrid.bakke@ntnu.no)

Master thesis in Biotechnology, 15, 30, 60 sp

Microbial control in land based recirculating aquaculture systems

Goal

The objective of this master thesis is to identify factors that are decisive for creating microbial stability in recirculating aquaculture systems.

Background

This master thesis will be part of the EU ERANET project MicStaTech, and the master student will work together with the project researchers. Water treatment and design of aquaculture systems are typically focused on optimising physicochemical water quality and efforts to maintain bacteria numbers low (i.e. by removing organic matter and disinfection). However, high bacteria numbers are not necessarily problematic for the cultured organisms as long as the system is bio-stable and all other requirements are met. In this project the main objective is to optimise the systems for microbial stability in the water instead of keeping low bacteria numbers, which has often been the main focus in RAS. This has implications for the technological solutions and optimal systems design. We are aiming at elucidating the underlying mechanisms to better understand the effects of water treatment on the microbial dynamics and for optimizing the microbial conditions for the reared fish.

Work description

The project will involve experiments for freshwater and seawater in lab-scale continuous reactors. Effects of for example different hydraulic retention times and biofilm area per volume on the development of microbial communities will be examined. The composition of the microbial communities in both biofilm and in the water will be studied by a 16S rDNA amplicon based strategy (DNA extraction, PCR, DGGE, DNA sequencing). Microbial numbers will be analysed by flow-cytometry, and also other water quality parameters will be measured.

Supervisors: Kari Attramadal Kari Attramadal (kari.attramadal@ntnu.no), Olav Vadstein (olav.vadstein@ntnu.no), and Ingrid Bakke (ingrid.bakke@ntnu.no)

Master thesis in Biotechnology, 60 sp

Microbial stabilization: a tool for combating pathogens in aquaculture systems?

Goal

To evaluate whether microbial stabilization is feasible a strategy to prevent blooming of pathogens in aquaculture systems.

Background

Fishes are sharing their living environment with high loads of bacteria. In nature, the fishes experience relatively stable microbial environments. In aquaculture systems, the reared animals are exposed to high and unstable loads of bacteria compared to the natural environments. For a number of reared marine species, we have previously demonstrated that stable microbial environments improve growth and survival. Stabilization of microbial communities in the rearing water can be obtained by so-called K-selection, i.e. keeping microbial loads close to the carrying capacity (the maximal microbial population size that the system can support). Recirculating aquaculture systems (RAS) are well suited for exerting microbial K-selection, because the water going in to the rearing tanks has a carrying capacity similar to that of the water inside the rearing tank. K-selected bacteria are typically specialists, characterized by low maximum growth rate, but with the ability to compete when the available resources are limited. In a system where the carrying capacity is dramatically increased in the rearing tank, e.g. by addition of fish feed in a flow-through system, rapid-growing, opportunistic bacteria will bloom. This would be an example of an r-selected system. R-selected bacteria have a high maximum growth rate, but are poor competitors when resources are limited. According to ecological theory, opportunistic rapid-growing bacteria would more easily bloom in an r-selected system with excess of resources, but would be outcompeted in a K-selected system.

If stabilization of the water microbial community is found to prevent blooming of opportunistic bacteria, this could be a promising and sustainable strategy for preventing pathogenic invasion in aquaculture systems.

Work description

This master thesis will be part of the EU ERANET project MicStaTech, and work closely together with the project researchers. We will use lab-scale continuous bioreactors for creating r- and K-selected microbial communities in both fresh- and marine water. Potential fish pathogens will be introduced to the systems under both K- and r-selected conditions, and the fate of these strains will be monitored by methods like qPCR and flow-cytometry combined with specific probing. For examining the dynamics of the microbial communities in the systems, methods based on analysis of sequence variation in the 16S rRNA gene will be used, like DNA sequencing and qPCR.

Supervisors: Ingrid Bakke, (Ingrid.bakke@ntnu.no) and Olav Vadstein (olav.vadstein@ntnu.no), Department of Biotechnology, Kari Attramadal (kari.attramadal@ntnu.no), Department of Biology

Production of therapeutic proteins in alternative bacterial species

Faglærer: Trygve Brautaset
Supervisor: Anne Krog (anne.krog@vectronbiosolutions.com), Tlf: 98404313,
Trond Erik Vee Aune (trond.aune@vectronbiosolutions.com), Tlf: 95027449

Background

Modern therapeutic proteins, such as insulin, are almost exclusively produced in *E. coli*. One of the challenges when producing recombinant proteins is solubility: a large fraction of the product is often found in an insoluble form, making it less useful for therapeutic applications.

The expression technology of Vectron Biosolutions was developed in *E. coli*, but can cover a broad range of bacterial species. By exploring the use of this technology in different bacterial species, the chances of finding a suitable production process for each protein is enhanced.

Project description

The goal of this project is to test and further develop the expression technology of Vectron Biosolutions for the production of proteins in alternative bacterial species.

Projects can be adjusted to fit different sp-profiles (15sp, 15+30sp or 60sp).

Tasks

Tasks depend on the final structure of the project, but will routinely include:

- Cloning of genes for therapeutic proteins into Vectron's vectors (PCR, gel electrophoresis, plasmid DNA isolation, plasmid purification, primer design).
- Transformation of *E. coli* with newly constructed vectors (make competent *E. coli* cells, transformation of *E. coli*)
- Using the expression of the reporter genes mCherry and beta-lactamase (growth experiments, enzyme activity assays).
- Expression of therapeutic proteins using the newly constructed vectors (bacterial growth experiments, protein isolation, SDS page, Western blot).
- Comparing the expression of the reporter genes and therapeutic proteins (bacterial growth experiments, protein isolation, SDS page, Western blot).
- Transferring the newly constructed vector into a new alternative host (transformation / conjugation / electroporation of alternative bacterial species).
- Comparing and evaluating the expression of soluble and insoluble protein fractions between *E. coli* and alternative hosts (bacterial growth experiments, protein isolation, SDS page, Western blot, protein (semi-)quantification).

About Vectron Biosolutions

Vectron Biosolutions is a small, dynamic company based at NTNU Gløshaugen. We provide state-of-the-art expression technology to both pharmaceutical and industrial companies worldwide. We welcome enthusiastic, independent students to further explore the possibilities our technology holds.

Reading

Brautaset, T., R. Lale, and S. Valla, *Positively regulated bacterial expression systems.* Microb Biotechnol, 2009. 2(1): p. 15-30.

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Biveileder/-e: *Co-supervisor/-s:*	Professor Olav Vadstein
Arbeidstittel på oppgaven/ *Preliminary title:*	**Molecular investigation of the beer brewing process**

Bakgrunn og mål / *Background and Objectives:*

Beer brewing is not only one of the oldest biotechnological processes; it is also one of the largest. In recent years there has been established many microbreweries in Norway but also the number of home brewers has increased significantly. Beer brewing is a complex biochemical and microbial process with many variables that affect the taste, aroma and overall quality of the finished product (e.g. type and composition of malted barley and other grains/ sugar-containing ingredients, development of bitterness and aroma by hop addition during various steps of brewing, water quality and adjustments, temperature profile during mashing, pre-condition and type of yeast, pitch number and fermentation temperature, maturation and storage). At IBT we are developing competence and conducting experiments on the microbial aspect of the beer brewing process with particular focus on challenges of the microbrewery industry. Currently we are investigating Norwegian Farmhouse Ale yeasts (kveik) at the genetic level and their beer fermentation properties. Another research project is sour beer production where combinations of yeast and lactic acid bacteria are used for studies of the development of the particular sour profile.

Eksperimentelt / *Experimental methods:*

Several brewings in the 30-50 l scale will be performed. Fermentations will be performed at 50 ml to 3 l scale. Analyses of the vort during the yeast fermentation, storage and finishing will be performed with mass spectrometric instrumentation (LC-MS, GC-MS incl dynamic head space injection) and other biochemical assays. Characterization of the flavor profiles as a function of the variables (e.g. yeast strains, fermentation conditions,..) both at sensory and analytical level will be of particular importance. Gene/ genome sequencing will be applied for the study of relationship between kveik (10 strains collected so far) and commercially available beer yeasts (both ale and lager yeast).

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Biveileder/-e: *Co-supervisor/-s:*	PhD candidate Lisa Marie Røst, IBT Professor Marit Otterlei, Department of Cancer Research and Molecular Medicine, NTNU
Arbeidstittel på oppgaven/ *Preliminary title:*	**Study of Carbon- and Energy Metabolism in Human Cancer Cells**

Bakgrunn og mål / *Background and Objectives:*

While abnormal metabolism of cancer has been known for over eighty years ("The Warburg Effect" – increased glucose consumption and lactate production) still much remain to be elucidated why and how cancer acquires this change in metabolism. Several recent discoveries have elucidated the role many common oncogenes and tumor suppressors play in reprogramming of metabolic pathways during oncogenesis, and lately it has been revealed that rewiring of metabolism in cancer is not only a consequence of hyper-activation of signaling pathways that instruct cells to grow, but that altered metabolism in itself can play a tumorigenic role. Thus, cancer metabolism is receiving renewed and increasing focus as therapeutic target.

Eksperimentelt / *Experimental methods:*

Mass Spectrometry (MS) is the most important technology to investigate metabolite pool (Metabolomics) and metabolic fluxes (Fluxomics) – two central analytical techniques to the study of the Carbon- and Energy metabolism of any biological system.

The main objective of the MSc project(s) is to perform stress response studies on human cancer cell lines using already established MS Metabolic Profiling methodology. The experimentation will comprise a number of well-known cancer cell lines combined with a number of cytostatics (e.g. DNA damaging agents) and other inhibitors of protein and cellular activity under hypoxic conditions, and monitoring the cellular stress response at the metabolite pool and metabolic flux levels (^{13}C experimentation). The expected achievement of the project is to generate more knowledge about cancer metabolism with potential identification of new cancer therapy targets.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 60 credits

Hovedveileder: *Main supervisor:*	Professor Per Bruheim
Kontaktinformasjon / epost *Contact information* / *email:*	Per.Bruheim@ntnu.no
Webside / *webpage*:	http://www.ntnu.no/ansatte/per.bruheim
Biveileder/-e: *Co-supervisor/-s:*	Post doc (to be hired summer 2016)
Arbeidstittel på oppgaven/ *Preliminary title:*	**Physiological studies of biofuel producing *Zymomonas mobilis***

Bakgrunn og mål / *Background and Objectives:*

This MSc project is associated the European Era-IB research project: "Z-Fuels: A novel bacterial system with integrated micro-bubble distillation for the production of acetaldehyde". The ultimate goal of Z-Fuels is to develop an integrated process in which low value waste (e.g. crude glycerol) is converted to a valuable biofuel and/or precursor chemical (acetaldehyde). The concept of Z-Fuels is to design, construct and operate a bacterial process, based on genetically engineered *Z. mobilis* with an integrated microbubble distillation system to convert complex sugary feedstocks and crude glycerol to acetaldehyde. Effective removal of acetaldehyde during the metabolic process will alleviate the inhibition and give higher yields. From the higher production quantities of acetaldehyde a more competitive and efficient route to butanol production can be obtained compared to current practise.

Eksperimentelt / *Experimental methods:*

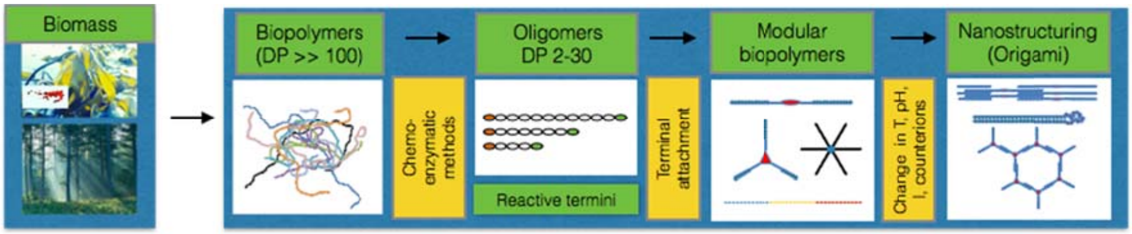
Bioreactor cultivations (100 mL to 2 L operating volume), sampling and sample processing for Metabolome and Fluxome (13C experimentation) analyses, mass spectrometric analysis (LC-MS, GC-MS, capIC-MS), enzymatic analysis and other biochemical assays (especially for studies of respiratory chain)

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 60 credits

Hovedveileder: *Main supervisor:*	Bjørn E. Christensen
Kontaktinformasjon / epost *Contact information / email:*	bjorn.e.christensen@ntnu.no
Webside / *webpage*:	http://www.biotech.ntnu.no/nobipol/BEC_homepage.php
Biveileder/-e: *Co-supervisor/-s:*	Ingrid Vikøren Mo
Arbeidstittel på oppgaven/ *Preliminary title:*	**New biopolymer hybrids by oligosaccharide conjugation**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*



The exploitation of biopolymers from carbon neutral biomass (wood, seaweeds, microorganisms) can be significantly increased and expand into novel applications (medicine, pharmacy, nanotechnology) by tailoring a new class of hitherto unexplored hybrid polymers. In brief, they are linear or branched constructs ($A_nB_mC_x$) of more than one oligomer [A, B or C (or more)] of predetermined lengths (n, m, x ..) (figure) combining through terminal coupling different self-assembling functionalities, aiming towards:

a) Nanoparticle formation (for drug delivery) in both aqueous and non-aqueous (lipophilic) systems
b) Dendritic-like structures for conjugation of oligosaccharide ligands to antibodies, proteins, aptamers etc. for targeted applications
c) Macroscopic biomaterials with tuneable nano- and microstructure (for cell proliferation and tissue engineering)
d) Self-assembling ‘block carbohydrate polymers’: Towards polysaccharide origami.
e)

Eksperimentelt / *Experimental methods:*

a) Controlled degradation of alginates to oligosaccharides
b) Oligosaccharide fractionation (gel filtration)
c) Terminal (reducing and non-reducing end) activation and conjugation
d) Analysis of conjugates (MS, NMR, chemical, chromatographic analysis)
e)

Note: Project starts up earliest 1. October 2016

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	15 ECTS project + 30 ECTS Master: MTKJ, MIKJ, MTNANO 60 ECTS: MBIOT5,
Omfang (studiepoeng): Credits (ECTS):	Flexible, dep. on study programme

Hovedveileder: *Main supervisor:*	Prof. Alexander Dikiy
Kontaktinformasjon / epost *Contact information* / *email:*	Tel: 73597863; alex.dikiy@ntnu.no
Webside / *webpage*:	http://folk.ntnu.no/dykyy/
Biveileder/-e: *Co-supervisor/-s:*	Dr. Elena Shumilina;
Arbeidstittel på oppgaven/ *Preliminary title:*	**Determination and analysis of novel bioactive compounds obtained from macro- and micro-algae**

Background and Objectives:
The aim of this project is to use NMR spectroscopy to determine industry relevant bioactive molecules from various algal extracts and to structurally characterise them.

Marine algae (contain a large amount of bioactive compounds (e.g. carotenoids, fucoidan, omega-3 and omega-6 fatty acids, pigments, amino acids, etc) that can be employed as pharmaceuticals, nutraceuticals, food additives, nutracosmeticals as well as for animal feed, fertiliser and biogas generation. The molecular content of different algae species differs greatly due to geography, time of the year and method of harvest and processing. However, little information is available on the most suitable harvesting time/geography and harvesting procedure to obtain the highest amount of bio-active compounds.

Experimental methods:
Within this project, several different extracts of algae will be studied using Nuclear Magnetic Resonance (NMR) in order to determine which bio-active compounds are present within them and measure their concentration. Certain bio-active compounds will be then further investigated and their structure determined using NMR.

No previous experience with the mentioned techniques is required.

The project results will be published in international scientific journal(s). We welcome students that have obtained relevant results to participate in the publication process as co-authors.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MSAQFOOD, MLREAL, MSBIO, MSMOLMED
Omfang (studiepoeng): Credits (ECTS):	60 credits

Hovedveileder: *Main supervisor:*	Prof. Alexander Dikiy
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Webside / *webpage*:	http://folk.ntnu.no/dykyy/
Biveileder/-e: *Co-supervisor/-s:*	Dr. Elena Shumilina
Arbeidstittel på oppgaven/ *Preliminary title:*	**Determination of quality metabolites in different brands of cod fillets**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*
The aim of the work is to determine the quality and molecular changes due to storage of different brands of cod fillets utilising Nuclear Magnetic Resonance (NMR).

Fish is an important nutritive source for human consumption. The world fish food supply has grown dramatically in the last years, with an average growth rate of 3.2 percent per year in the period 1961–2009 (FAO, 2012). Atlantic cod (Gadus morhua) is a popular food product in Norway and worldwide.

Different companies sell cod of varying qualities. For the consumer it is important to know whether the price correlates with the quality of the product and how and for how long the fish should be stored, in order to keep all the metabolites that account for its health benefits.

Eksperimentelt / *Experimental methods:*
Within this project, the student will utilise a method developed in our laboratory to test A) the quality (amount of vitamins, amino acids, fatty acids, etc.) of cod purchased from different producers utilising NMR spectroscopy; B) characterise how these products change their metabolic profile over time and C) characterise how their metabolic profile changes depending on storage temperatures and time.

No previous experience with the mentioned techniques is required.

The project results will be published in international scientific journal(s). We welcome students that have obtained relevant results to participate in the publication process as co-authors.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MSAQFOOD, MLREAL, MSBIO, MSMOLMED
Omfang (studiepoeng): Credits (ECTS):	60 credits / 30 credits

Hovedveileder: *Main supervisor:*	Prof. Alexander Dikiy
Kontaktinformasjon / epost *Contact information* / *email:*	alex.dikiy@biotech.ntnu.no
Webside / *webpage*:	http://folk.ntnu.no/dykyy/
Biveileder/-e: *Co-supervisor/-s:*	Dr. Elena Shumilina
Arbeidstittel på oppgaven/ *Preliminary title:*	**Development of a methodology to determine frauds in salmon products**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*

The aim of the work is to develop a method and protocol to determine salmon frauds utilising Nuclear Magnetic Resonance (NMR).

Fish is an important nutritive source for human consumption. The world fish food supply has grown dramatically in the last years, with an average growth rate of 3.2 percent per year in the period 1961–2009 (FAO, 2012). Atlantic salmon (Salmo salar) is a popular food product in Norway and worldwide due to its delicate taste and health benefits obtained from its metabolites (peptides, carbohydrates, vitamins, lipids).

However, as it happens with different fish, salmon products can be counterfeit to sell a lower quality product for a higher price. Several methods exist on how to determine frauds in fish, such as genetic verifications, isotope analysis, etc. However, most of them have several limitations.

Eksperimentelt / *Experimental methods:*

Within this project a method will be developed that will allow the detection of fraud products utilising NMR spectroscopy. Firstly, a model of salmon metabolites will be made by analysing both fresh and frozen samples of the fish. Subsequently, various frauds will be purposefully created to assess the validity of the developed methodology. The final stage of the project will be to create a protocol that might be used by authorities to detect counterfeits.

No previous experience with the mentioned techniques is required.

The project results will be published in international scientific journal(s). We welcome students that have obtained relevant results to participate in the publication process as co-authors.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MSAQFOOD, MLREAL, MSBIO, MSMOLMED
Omfang (studiepoeng): Credits (ECTS):	60 credits / 30 credits

Hovedveileder: *Main supervisor:*	Prof. Alexander Dikiy
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Webside / *webpage*:	http://folk.ntnu.no/dykyy/
Biveileder/-e: *Co-supervisor/-s:*	Dr. Elena Shumilina
Arbeidstittel på oppgaven/ *Preliminary title:*	**Determination of stress biomarkers in human saliva**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*

The aim of this project is to determine which molecules in human saliva correlate with stress and can be thus used as biomarkers.

Stress is a condition that affects both body and mind of people. High levels of stress trigger changes in the metabolism, hormonal levels and physiological reactions. Stress is currently mostly monitored by analysing the concentration of the hormone cortisol in blood. However, such method is invasive, costly, requires specialised personnel for collection and if carried out with not sterile equipment can result in contamination with diseases. Presently, methods that are non-invasive are gaining popularity, such as the analysis of cortisol in saliva samples. For such purpose an enzyme-linked immunosorbent assay (ELISA) is usually used. However, such method is relatively time consuming and as result gives the concentration of only one molecule in the sample.

Eksperimentelt / *Experimental methods:*

Within this project, it will be investigated whether other molecules can be found in saliva samples that change in quantity depending upon stress levels. In order to study a high number of molecules, Nuclear Magnetic Resonance (NMR) spectroscopy will be used. Saliva samples of stressed and not stressed people will be analysed both by NMR and by ELISA and the results will be compared.

The results of such research may help find an efficient and fast way to detect stress both in humans and animals.

No previous experience with the mentioned techniques is required.

The project results will be published in international scientific journal(s). We welcome students that have obtained relevant results to participate in the publication process as co-authors.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MSAQFOOD, MLREAL, MSBIO, MSMOLMED
Omfang (studiepoeng): Credits (ECTS):	60 credits

Hovedveileder: *Main supervisor:*	Helga Ertesvåg
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Biveileder/-e: *Co-supervisor/-s:*	
Arbeidstittel på oppgaven/ *Preliminary title:*	**Polysaccharide production in *Azotobacter vinelandii* cysts**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*

Azotobacter vinelandii is a gram-negative bacterium that will enter a resting stage called cyst upon encountering adverse growth conditions. I have performed a transcriptome study and identified two gene clusters probably involved in producing polysaccharides that are expressed during encystment. No one knows which polysaccharides the clusters are involved in producing.

As a first attempt at unraveling what these genes are doing, I would like to inactivate one gene in each of these gene clusters and analyse the effect on encystment. Avin05390 and Avin30120 are the best candidates for genes to target. For a project work making the constructs in *Escherichia coli* and transferring the plasmids to *A. vinelandii* will be a realistic aim, it will then be possible to continue the work in a 30 stp project.

Eksperimentelt / *Experimental methods:*

1. Construct the recombination vectors (The standard techniques: Cloning, PCR, sequencing)
2. Transfer the vectors to *A. vinelandii.*
3. Select and validate mutants.
4. Show if and how the mutation affects encystment
5. Use bioinformatic tools to present a hypothesis as to which polysaccharides the clusters are producing.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Hovedveileder: *Main supervisor:*	Helga Ertesvåg
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Biveileder/-e: *Co-supervisor/-s:*	
Arbeidstittel på oppgaven/ *Preliminary title:*	**Heterologous expression of large gene clusters**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*

It is no fairly straight forward to clone a gene encoding a single protein and express that protein. Cloning of large gene clusters encoding a pathway is more of a challenge, and to actually obtain the product expected from that pathway is an achievement to be proud of. Still, methods for cloning large DNA fragments and expressing them in other bacteria have been published [1]. I would like to establish this method in my group, and propose to use a putative alginate biosynthetic cluster from the bacterium *Marinobacter algicola* as the model gene cluster.

Eksperimentelt / *Experimental methods:*

1. Use the published method to clone the cluster in such a way that it is controlled by an inducible promoter. The recombinant plasmid will then have to be characterized using restriction enzyme analysis and DNA sequencing. A 15 stp project will probably not get further.

2. Test if the plasmid is sufficient to get some alginate production in a: *Pseudomonas fluorescens*, which is a bacterium we know has the ability to produce the polymer; b: *M. algicola*; c: *Escherichia coli*. The procedure for plasmid transfer, growth of these bacteria and alginate assays are well established in the laboratory.

3. A 60 stp project would probably also include using the method to clone other gene clusters.

Reference:

1. Gemperlein K, Zipf G, Bernauer HS, Muller R, Wenzel SC: Metabolic engineering of *Pseudomonas putida* for production of docosahexaenoic acid based on a myxobacterial PUFA synthase. *Metab Eng* 2016, 33:98-108.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Hovedveileder: *Main supervisor:*	Helga Ertesvåg
Kontaktinformasjon / epost *Contact information* / *email:*	helga.ertesvag@ntnu.no
Webside / *webpage*:	http://www.ntnu.no/ansatte/helga.ertesvag
Biveileder/-e: *Co-supervisor/-s:*	
Arbeidstittel på oppgaven/ *Preliminary title:*	**Develop *Rhodococcus opacus* as a platform organism for lipid production**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*

Rhodococcus opacus is an actinomycete that is able to store large amounts of lipids in lipid bodies within its cytoplasm. At NTNU it has been chosen as one contender in a project aimed at producing the essential omega-3 fatty acids DHA and EPA for aquaculture feed. Aquaculture is the most likely way of providing animal protein for the increasing human population, and new sources for omega-3 are necessary in order to increase the production from aquaculture.

In connection with the ongoing MIRA project it is possible to define molecular biology projects tailored to the wishes of the student. Topics could be: optimized vectors and methods. Cloning and characterization of specific proteins like acetyl transferases, elucidation of gene function, making specific gene knock-outs etc. Literature studies or bioinformatic studies could also be included as part of the project.

Since this is a very open project, it will be available for up to three students. Each will be given their separate project. These projects will be specified in a dialog between the student and the supervisor, and will also depend on how far the MIRA project has developed when the individual students are starting up their thesis work.

Eksperimentelt / *Experimental methods:*

The techniques utilized will vary with the actual topic for and length of the project. All will contain standard techniques (Cloning, PCR, DNA sequencing). Other possible experiments might be: construction and characterization of new strains, vector construction/characterization or protein purification and characterization.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Hovedveileder: *Main supervisor:*	Martin Hohmann-Marriott
Kontaktinformasjon / epost *Contact information / email:*	martin.hohmann-marriott@ntnu.no
Webside / *webpage*:	www.photosynlab.org
Biveileder/-e: *Co-supervisor/-s:*	Rahmi Lale (Biotechnology) Murat Adelan (Biology)
Arbeidstittel på oppgaven/ *Preliminary title:*	**Nanowire-mediated electron transport by bacteria** **- Molecular mechanisms** **- Ocean productivity** **- Biological solar cells**

Background and Objectives:

Cyanobacteria make protein filaments that function as electrical wires, «nanowire». We are now just starting to understand why cyanobacteria make these nanowires. Electron transport to metal oxides is enabling cyanobacteria to respire in the absence of oxygen, but also allows the acquisition of metals that are required for growth. These metabolic functions have important consequences for the geobiochemistry and species distribution in oceans. In addition, understanding the molecular components involved in nanowire functionality provides a blueprint for developing biophotovoltaic solar cells.

Experimental methods:

Depending on the student's interest this project may include: Molecular biological techniques (cloning, PCR, etc), physiological techniques (growth analysis, oxygen measurements), analytical techniques (metal analysis), microbiological techniques (sterile & culturing techniques), bioinformatics, spectroscopy (absorption and fluorescence), electronics/electrophysiology (instrument design, programming, potentiometry).

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MSBIO, MBIOT5, MSBIOTECH, MSPHYS, MTNANO
Omfang (studiepoeng): Credits (ECTS):	30 or 60 studiepoeng

Hovedveileder: *Main supervisor:*	Adjunct Assoc. Prof. Rahmi Lale
Kontaktinformasjon / epost *Contact information / email:*	rahmi.lale@ntnu.no
Webside / *webpage*:	http://www.photosynlab.org
Biveileder/-e: *Co-supervisor/-s:*	Assoc. Prof. Vasili Hauryliuk, Umeå University, Sweden; The Laboratory for Molecular Infection Medicine Sweden within the Nordic EMBL Partnership for Molecular Medicine http://www.mims.umu.se/groups/vasili-hauryliuk.html
Arbeidstittel på oppgaven/ *Preliminary title:*	***In vitro* Translation with Engineered Ribosomes**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:* Protein synthesis by ribosomes is present in all three domains of life rendering it as a crucial process. Ribosomes are composed of two subunits, each built on a separate ribosomal RNA (rRNA) scaffold. In recent years synthetic biology effort has led to breakthrough applications of engineered ribosomes: 'orthogonal' ribosomes that can only 'read' a designer 'orthogonal' mRNA and can incorporate unnatural amino acids (PubMedID 24755590); 'tethered' ribosomes with the two subunits conjoined into a single artificial rRNA molecule (PMID 26222032); 'tagged' ribosomes for selectively purification on one-step affinity chromatography (PMID 19074194).

The Goal of the project is to engineer and purify affinity-tagged tethered ribosome to be used in *in vitro* translation kits. As a next step we will attach elongation factor G (EF-G) to the affinity-tagged tethered ribosome, which will allow one-step purification of a minimalistic *in vitro* translational system for biotechnological applications.

Eksperimentelt / *Experimental methods:* The project relies on expertise of the host laboratory in **synthetic biology** (Dr. Lale) and **bacterial protein synthesis** (Dr. Hauryliuk). The first step is a construction of panel of plasmid expression vectors for inducible expression of non-essential ribosomal protein S9, extended with several variants of poly-His affinity tag, for one-step purification. The optimal construct will be selected by testing expression of chimeric proteins in *E. coli* strain lacking the genomic copy of S9 and testing ribosomal isolation on affinity columns. The second step is fusing the best performing His-tagged S9 construct with elongation factor G (EF-G) via a flexible GS-rich linker. Engineered ribosomes will be purified on affinity chromatography and characterized using *in vitro* translation system. Best-performing constructs will be integrated into *E. coli* genome creating the final strain.

The project will utilize the following **Techniques**: 1) cloning using synthetic biology techniques such as ligase cycling reaction; 2) bacterial genome engineering using λ Red recombineering; 3) protein detection using Western blotting; 4) affinity purification using Immobilized-metal affinity chromatography; 5) biochemical assays in *in vitro* translational system.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng 60 credits

Hovedveileder: *Main supervisor:*	Turid Rustad
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Webside / *webpage*:	
Biveileder/-e: *Co-supervisor/-s:*	Ulf Erikson, SINTEF
Arbeidstittel på oppgaven/ *Preliminary title:*	**Bestemmelse av kvalitetsendringer i fisk ved bruk av ny metodikk**

Bakgrunn og mål / *Background and Objectives:*

Det er et økende salg av frossen tint fisk. Denne selges også som fersk. Det er derfor behov for målemetoder som kan skille mellom fersk og frossen tint fisk. Noen målemetoder finnes – men disse er tidkrevende og lite presise. For å kunne forbedre og utvikle nye og bedre prosesseringsmetoder for bla fisk er det behov for gode målemetoder for å bestemme endringer i råstoffet som funksjon av prosessbetingelser. Dette vil for eksempel være å bestemme når proteindenatureringen begynner – bla ved varmebehandling – hvis vi ønsker mildere varmebehandling – hva skjer med proteinene (og tekstur med mer). Det er også mulig å studere effekt av ulike tinemetoder osv.

Eksperimentelt / *Experimental methods:*

Oppgaven vil gå ut på å bruke måle endringer i proteiner ved hjelp av endringer i overflatespenning ved hjelp av et nytt utviklet instrument og koble dette til målinger med konvensjonelle metoder.
Det vil bli gjort målinger på fersk fisk som er behandlet på ulik måte, fersk, lagret og frossen tint. Prøvene vil bli analysert ved hjelp av overflatespenningsmetoden og ved metoder slik som endringer i proteinløselighet, vannbindingsevne, tekstur og evt endringer i enzymaktivitet.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ
Omfang (studiepoeng): Credits (ECTS):	15 studiepoeng

Hovedveileder: *Main supervisor:*	Turid Rustad
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Webside / *webpage*:	
Biveileder/-e: *Co-supervisor/-s:*	Revilija Mozuraityte, SINTEF Fisheries and Aquaculture
Arbeidstittel på oppgaven/ *Preliminary title:*	**Processing to retain quality and stability of healthy nutrients in model mackerel products**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*

The aim of this work is to optimize the processing steps of model products from mackerel. Re-formulated products (mimics fishcake/finger) will be made and Sous vide (light heat treatment) will be used. The focus will be on the quality and stability of healthy nutrient like omega – 3 fatty acids.

Consumption of fatty fish such as mackerel provides numerous important nutrients linked both to their lipids, proteins and water soluble components. The lipids in mackerel are rich in long chain n-3 polyunsaturated fatty acids (LC n-3 PUFA) with well documented beneficial effects e.g. on cardiovascular diseases. However, the LC n-3 PUFA are highly susceptible to oxidation resulting in rapid quality loss such as reduced sensory quality (undesirable taste and flavour) of the product. **This work will screen the changes in lipids during processing of mackerel into model ready to eat/sous vide mackerel products.** The ability of natural antioxidants like herbs to increase the oxidative stability of the model products will be studied.

Eksperimentelt / *Experimental methods:*

The methods involved in the study will be mainly: compositional analysis (lipid, water, protein content) and quality analysis (amount of peroxides, conjugated dienes, thiobarbituric reactive substances and free fatty acids). Additional investigation on the lipid oxidation methods will be carried out in order to choose and optimise the available methods for the analysis of marinated herring.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Hovedveileder: *Main supervisor:*	Turid Rustad
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Webside / *webpage*:	
Biveileder/-e: *Co-supervisor/-s:*	Jørgen Lerfall, IMAT
Arbeidstittel på oppgaven/ *Preliminary title:*	**Storage quality of ready-to-eat Atlantic salmon treated with soluble gas stabilization (SGS)-technology and gentle heating**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*

For å øke inntak av sjømat er det behov for utvikling av attraktive, stabile og velsmakende produkter. Det vil si produkter som er lettvinte å bruke og har god holdbarhet. For å utvikle slike produkter er det nødvendig med mer kunnskap både om råstoffene som skal inngå og hvordan disse påvirkes av prosess og lagring samt om hvordan prosessering og ingredienser påvirker holdbarhet. Oppgaven går ut på å optimalisere kombinasjonen av SGS- og varmebehandling av Atlantisk laks for å sikre god kjemisk og mikrobiell holdbarhet av laks. Ulike SGS betingelser (tid, temperatur, emballasje), varmebehandling (type, temperatur + tid kombinasjon) vil bli studert. Spesielt for varmebehandling vil man se på hvordan kvaliteten av laksen påvirkes ved lett varmebehandling samt hvilke varmebehandlingsmetoder som kan benyttes. I tillegg vil man måle hvor mye varmebehandlingen påvirker innløsningen av CO_2.

Eksperimentelt / *Experimental methods:*

SGS-teknologi vil bli testet i kombinasjon med forskjellige varmebehandlinger. Hvor mye CO_2-som blir løst opp vil bli bestemt. For å følge kvalitetsendringer vil mikrobiell, kjemisk og/eller fysikalsk kvalitet ved forskjellige behandlinger (enkeltvis og i kombinasjon) bli bestemt.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Arbeidstittel på oppgaven/ *Preliminary title:*	**Characterization of waste streams**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*
A large amount of food raw material is wasted at different stages through the value chain. Currently the waste streams within the food processing factory underlie partly treatment and recycling, but finally all remaining waste streams are disposed as one single waste stream. The project Biosuck aims to reduce the food waste streams in the processing industry. To utilize valuable components in the waste streams there is a need for characterization of the composition of these streams. At NTNU we will analyze representative samples of waste streams with chemical and biochemical methods.

Since the described thesis is highly innovative it is expected that some relevant data can be published in peer review journals.

Eksperimentelt / *Experimental methods:*
Representative samples of waste streams with chemical and biochemical methods.

Selected samples will be analyzed by spectral methods like NMR (NMR structural elucidation and NMR metabolic profiling) and MALDI TOF-TOF. These innovative methods shall help to identify new and more efficient ways to analyze waste samples and to simplify the categorization of possible bioactive compounds or i.e. enzymes isolable from the waste streams. These investigations will contribute to the increasing value creation out of the waste streams.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Biveileder/-e: *Co-supervisor/-s:*	Rasa Slizyte og Kirsti Greiff
Arbeidstittel på oppgaven/ *Preliminary title:*	**Funksjonelle ingredienser i mat**

Hovedmålet med oppgaven vil være å undersøke hvilke effekter tilsetning av ulike ingredienser har på fysio-kjemiske, sensoriske og teknologiske egenskaper i mat.

Bakgrunn og mål:

Enzymatisk hydrolyse er en prosesseringsteknikk som kan benyttes for å produsere høyverdige ingredienser fra restråstoff. Prosessen er basert på bruk av kommersielle enzymer (proteaser) som bryter peptidbindinger, forenkler degraderingen av råstoffet og fører til utskillelse av oljen. Resultatet er tre fraksjoner; proteinhydrolysat (vannløselig protein), olje og grakse (uløselig proteiner, fosfolipider og bein). Råstoffsammensetning, enzymtype og prosessbetingelsene vil påvirke egenskapene til sluttproduktene, noe som gjør det nødvendig å utvikle prosesser skreddersydd for det restråstoffet det er tenkt brukt på. SINTEF Fiskeri og havbruk har gjennom flere prosjekter utviklet teknologier for utnyttelse av restråstoff fra fisk og kylling. Et resultat av dette er ulike ingredienser som kan ha funksjonelle egenskaper ved prosessering av mat, gi økt næringsverdi og påvirke sensoriske og teknologiske egenskaper i ferdig produkt.

Eksperimentelt*:*

Prosjektarbeidet vil bli knyttet opp mot aktiviteter som SINTEF Fiskeri og havbruk har i prosjekter på dette området. Det vil være behov for forsøk og analysering av både ingredienser og ferdig produkt.

Aktiviteter som kan inngå i dette prosjektet:

- Karakterisering av kjemisk sammensetning i ingrediensene
- Pilotforsøk hvor modellprodukter testes ut
- Fysio-kjemiske, sensoriske og teknologiske analyser.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Biveileder/-e: *Co-supervisor/-s:*	Alex Dikiy, Rasa Slizyte/Revilija Mozuraityte (SINTEF)
Arbeidstittel på oppgaven/ *Preliminary title:*	**Technological solutions for production of safe and high quality proteins from salmon rest raw materials**

Bakgrunn og mål / *Background and Objectives:*

Rest- and by-products from slaughtering and processing of farmed salmon contain valuable protein and lipid as well as vitamins and minerals. Today, most of these by-products goes to low value fish silage for use as animal feed. The slaughtering and processing of the farmed fish generate fresh, high quality rest- and by-products that may be separated into different fractions. These raw materials therefore has great potential to be used for products to more demanding, but also better paying markets such as ingredients, e.g. protein hydrolysates, for use in functional stage specific diets for poultry, pet food including nutritional supplements for human consumption. This requires hygienic handling of the by-products to ensure food safety as well as methods to generate storage-stable products.

One of the most fundamental challenges are decomposition of rest raw material and formation of undesirable compounds like biogenic amines (BAs) such as histamine, tyramine, putrescine, cadaverine and phenylethylamine in poorly stored raw materials or later during processing. The overall project idea is to develop **technological toolbox to control safety, quality and stability of proteins from salmon rest raw materials for dietary functional application**. The technological toolbox will include the solutions to prevent formation of undesirable components (BA), microbiological control and establishing product stability through the processing chain.

Eksperimentelt / *Experimental methods:*

*Experimental part will cover de*fining raw material composition, storage as well as processing parameters for production of safe and high quality products to be used in functional applications as high value ingredients.

This will involve:

- Determination of chemical composition of raw material
- Characterization of degradation products (including biogenic amines) by traditional and rapid analytical techniques like NMR
- Identification where during different technological steps, undesirable components are formed.
- Identification the stability of the protein concentrate as a function of dry matter, pH, degree of hydrolysis and storage temperature.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Biveileder/-e: *Co-supervisor/-s:*	Pierrick Stevant
Arbeidstittel på oppgaven/ *Preliminary title:*	**Extraction of fucoxanthin from macroalgae**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*
Macroalgae or seaweed is a biomass resource that can be utilized for food, feed, chemicals and energy. Today the main use of seaweed in Norway is for extraction/production of hydrocolloids. However macroalgae also contains valuable proteins as well as other components including bioactive compounds. Norway has a long coastline and good possibilities not only to harvest but also to grow macroalgae. In Norway, kelp is extensively harvested for alginate production, but macroalgae have not been significantly appreciated as food or for other applications. However, more recently cultivation of macroalgae for a wider range of potential product applications has been predicted. In addition to hydrocolloids, proteins and minerals, brown algae also contains bioactive compounds such as the carotenoid fucoxanthin which can have antioxidant effect and that has been shown to promote fat burning within fat cells in white adipose tissue.

Eksperimentelt / *Experimental methods:* The task will be to test different methods to extract the fucoxanthin and to determine the antioxidant effect.
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Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Arbeidstittel på oppgaven/ *Preliminary title:*	**Quality changes of macroalgae during preservation and processing**

Bakgrunn og mål / *Background and Objectives:*

Much of future human food supply is predicted to originate from the world's oceans. Throughout the past decades, use of marine macroalgae ('seaweed') in food production has undergone a renaissance in the western world, as seaweeds offer potential solutions in the context of global climate change and environmental challenges. In comparison with terrestrial biomass, seaweeds are produced without demands on soil, fresh water or land area.

Macroalgae have been eaten by humans for thousands of years and have been used in animal production as sources of nutrients and health-promoting compounds since the domestication of animals. This long history of use reflects macroalgal qualities: many species contain proteins with well-balanced amino acid composition at levels high enough to make them useful as protein sources for humans and animals. Macroalgae may also be important sources of minerals, such as iodine, iron and calcium; ingredients which are often limiting in traditional food sources. With its extensive coastline and existing knowhow on processing of marine raw materials and related infrastructure, Norway is a prime candidate for developing a bio-economy based on cultivation and processing of seaweeds.

Due to the high water content and easy degradable component in macroalgae, preservation is required for transportation and storage, and this step is critical for quality of raw materials and ingredients obtained by followed processing. Primary treatment which are known to affect raw material characteristics and content of both beneficial as well as non-desirable components include washing (rinsing/soaking), preservation by pH or dehydration (e.g. air drying/ freeze-drying), maturation and storage. For production of food and feed ingredients, fractionation of the biomass is required. A main challenge for protein extraction will be the presence of gel-forming polysaccharides, due to their high-water binding capacity and viscosity. It is important to evaluate how initial treatments/preserving influence the quality and following processing/fractionation of macroalger.

Eksperimentelt / *Experimental methods:*

Experimental part will cover several preservation/stabilisation methods after harvesting of macroalger:

- *Freezing*
- *Drying*
- *Preservation by pH*

The following quality indicators will be evaluate after preservation steps:

- Changes in chemical composition of raw material
- Microbiological quality
- Influence of following processing and fractionation of microalger

Passer for (angi studieretning/hovedprofil/-er): *Suitable for main profiles:*	Feks MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Biveileder/-e: *Co-supervisor/-s:*	Grete Hansen Aas Kristin Bjørdal
Arbeidstittel på oppgaven/ *Preliminary title:*	**Marine protein ingredients in functional food**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*
Fish rest raw material is mainly used for production of feed. Processing into products/ingredients for human consumption will increase profitability. The local industry at Møre has started the production of protein meal from rest raw material both from herring and white fish. Human consumption of the valuable fish proteins are depending on finding a good way to administer this. How these powders may be suited to increase protein content in different foods is not well described. They may be added to different processed seafood or administered in liquids for nutrient drinks/sports nutrition. Different protein ingredients are available for testing.

The aim of this study is to test different ways to administer these fish powders, and to test how this addition will affect the functional properties as well as the sensory properties of the products. This study can also be extended to include marine lipids.

Eksperimentelt / *Experimental methods:*
The task will be to find a suitable model product and test inclusion of different levels of protein. The functional properties (water holding, texture ..) and quality measured by sensory attributes will then be tested.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH eller MSAQFOOD
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

Hovedveileder: *Main supervisor:*	Marit Sletmoen
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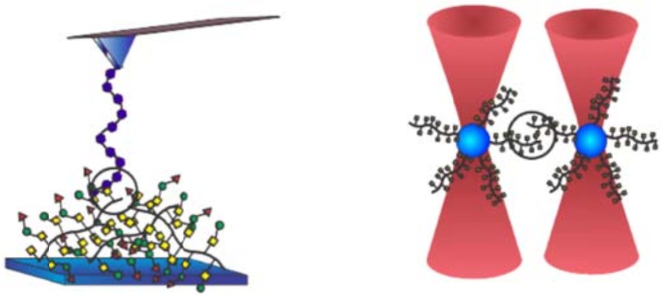
Biveileder/-e: *Co-supervisor/-s:*	Gianfranco Picco, Kings College, London.
Arbeidstittel på oppgaven/ *Preliminary title:*	**Carbohydrate antigens in human health and disease**

Short description of the project:

Background and Objectives:

The recognition of specific carbohydrate chains (glycans) by carbohydrate-binding proteins (lectins) is an important regulatory mechanism in healthy and diseased immune physiology.

We are investigating the effect of the aberrant glycosylation occurring in the majority of human cancers. We are currently investigating how certain carbohydrate based tumor-associated antigens interact with specific lectins found on antigen presenting cells. The interactions investigated are believed to have consequences for the further progression of the cancer.



Biomacromolecules to be investigated are immobilized onto flat surfaces for investigations using AFM microscopy (left) or onto the surface of polystyrene beads for investigation using optical tweezers (right).

Experimental methods:

The main experimental approach will be the direct determination of glycan interactions using the sensitive force probes atomic force microscopy (AFM) or optical tweezers (OT). These techniques allow determining intermolecular interaction forces with picoNewton resolution. They are thus powerful tools to provide new information concerning specific biological interactions.

The topic can be adjusted to fit with the expected workload for 60, 30 or 15 credits.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MTNANO
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Biveileder/-e: *Co-supervisor/-s:*	Kjell Morten Vårum Etienne Dague and Helene Martin-Ykes, LAAS, Toulouse, France
Arbeidstittel på oppgaven/ *Preliminary title:*	**Mode of action of antimicrobial agents**

Short description of the project:

Background and Objectives:

The awareness for safer control of microbial stability in food and pharmaceutical systems is today increasing. Successful transformation from synthetic pesticides to more environmentally friendly ones and techniques enabling their reduced use while at the same time ensuring healthy plants requires both identification of alternative pesticide candidates and the establishment of robust structure activity relationships.

Natural products are an excellent alternative to synthetic pesticides as a means to reduce negative impacts to human health and the environment. Unfortunately, the limited knowledge concerning the mode of action of the natural products as well as their precise effect on different systems hampers their use and their potential is thus not fully released. We are interested in increasing the understanding of both how currently used synthetic pesticides provide their effect as well as to initiate the development of a necessary knowledge base for the natural product chitosan as an antibacterial and antifungal pesticide.

Experimental methods:

Fumonicin is one much used antimicrobial agent that is relevant to study. Additionally, a library of well-defined chitosan samples with a range of molecular parameters (M_w, M_w-distribution and D_A) are available. These samples host interaction capacities based on their cationic and hydrophobic nature, with interaction strength controllable by their molecular parameters. The bacterium *Escherichia coli* and the yeast ***Saccharomyces cerevisiae,*** **are relevant microorganisms to be used to demonstrate structure – antimicrobial activity.**

Conclusions concerning the effect of chitosan on the viability of the different microorganisms will be based on studies of cells prior to and after exposure to the antimicrobial agent. The observed interaction between positively charged molecules, including chitosan, and the surface of bacteria is most likely due to electrostatic interaction with negatively charged lipopolysaccharides. Deposition of chitosan leads to thickened cell envelope and blocking of the nutrient flow with concomitant cell death. We hypothesize that early effects of chitosan can be monitored by changes in cell volume, morphology and mechanical properties. Relevant experimental tools to monitor these changes include divers' forms of microscopy as well as direct determination of mechanical properties of the cells using the sensitive force probe AFM.

The topic can be adjusted to fit with the expected workload for 60, 30 or 15 credits.

Suitable for main profiles:	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MTNANO
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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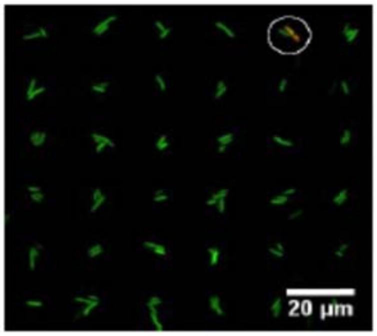
Biveileder/-e: *Co-supervisor/-s:*	Etienne Dague and Helene Martin-Ykes, LAAS, Toulouse, France
Arbeidstittel på oppgaven/ *Preliminary title:*	**Preparation and study of cellular microarrays**

Short description of the project:

Background and Objectives:

We have developed bacterial microarrays that can form the basis for efficient studies of heterogeneity within populations of bacteria. However, such microarrays could also be prepared for also other forms of microorganisms. The display in microarrays is for example relevant for efficient studies of the effect of changing external parameters on the behaviour of fungi or yeast.



Bacterial microarrays observed using fluorescence microscopy.

We are interested in studying the effect of antibiotics as well as other forms of antimicrobial agents on the behavior of bacteria and yeast cells. The investigation of the mode of action of these antimicrobial agents could benefit from the preparation of ordered arrays of bacteria or yeast cells, allowing efficient experimental studies, including microscopic tracking, of the influence of the added compounds on the cells.

Experimental methods:

The work will include some or all of the following tasks:

- Preparation of PDMS stamps needed for deposition of chemicals in spots on glass surfaces. The stamps will be prepared using lithographic tools available in NTNU Nanolab.
- Identification of optimal surface functionalization for immobilization of the relevant bacterium or yeast cells.
- Studies of microarrays using fluorescence or light microscopy.
- Studies of microarrays using quantitative phase contrast microscopy.

The topic can be adjusted to fit with the expected workload for 60 or 30 credits.

Suitable for main profiles:	MTKJ/MIKJ, MBIOT5, MSBIOTECH, MTNANO
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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Biveileder/-e: *Co-supervisor/-s:*	Finn Aachmann
Arbeidstittel på oppgaven/ *Preliminary title:*	**Alginate matrices for tissue engineering**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*

Alginate is a attractive biopolymer for use as scaffold (matrix) in tissue engineering. Although alginate entrapment is a very gentle technique for immobilizing living cells, many cells need specific interaction with the matrix for their proliferation and viability. Such anchoring depending behaviour is common for most mammalian cells and the alginate network itself is non-interacting. Peptides known from the extracellular matrix (ECM) to interact with integrins in the cell membrane can be linked to alginate and induce attachment of cells to the alginate. Interactions between ECM and integrins have been shown to determine cell morphology, viability and differentiation, and is thus highly relevant study objects in tissue engineering. Of particular interest is the covalent linkage of peptides that can be used to crosslink the alginate and that cells by secreted enzymes can degrade and by this modify their microenvironment. **The aim of the project is to design novel alginate matrices covalent cross-linked with peptides that can be degraded by proteases and with cell adhesion properties.**

Eksperimentelt / *Experimental methods:*

Different peptides will be covalently link to alginate using a novel method developed at IBT, NTNU. NMR spectroscopy, light scattering (SEC-MALS) and viscosity measurements, will be relevant method for product characterisation (e.g. degree of coupling and crosslinking). Hydrogel properties, such as gel elasticity and stability will be studied. Studies of cell interactions with the developed materials on 2D gels and in 3D gels using confocal microscopy may be a part of the project depending on the student interests and the progress of the project.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	60 studiepoeng / 30 sp studiepoeng / 15 studiepoeng 60 credits / 30 credits / 15 credits (specialization project)

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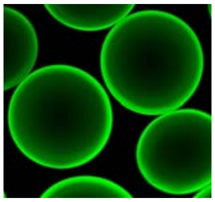
Biveileder/-e: *Co-supervisor/-s:*	Abba E. Coron
Arbeidstittel på oppgaven/ *Preliminary title:*	**Strategies for stabilising alginate beads of intermediate G content**

Project description:

Alginate microbeads have through many years of research shown great potential as an immunoisolation system for the entrapment of insulin-producing cells. The preferential use of alginate gels in cell immobilisation is primarily due to the gentle environment they provide for the entrapped material. Alginate is a binary heteropolymer containing 1,4-linked β-**D**-mannuronic acid (M) and α-**L**-guluronic acid (G) residues, known for its gel forming properties in the presence of divalent cations. The use of alginate gels for cell encapsulation provides many challenges related to its application, which includes destabilisation of the gel network in terms of swelling and gel dissolution, as well as increased pore size, at physiological conditions (Mørch et al., 2006). Traditionally, a polycation layer has been applied to stabilise the alginate gel beads. However, the conventional polycation layer (poly-L- lysine) has been found to be highly immune stimulating, associated with cellular overgrowth on the surface of the alginate capsule (Strand et al., 2001), in addition to activating the complement system (Rokstad et al., 2011). The functional properties of alginate are essentially governed by the content of M and G. In a recent *in vivo* study performed by Tam et al. (2011), alginate isolated from *Laminaria hyperborea* leaf with an intermediate G content was found to be biocompatible. However, the alginate displayed a low degree of stability in terms of swelling and bead fragmentation upon transplantation.

The aim of the current project, with the possibility of a continuation to a master's project, is to explore different strategies for stabilising alginate beads made from *L. hyperborea* leaf alginate, which has already shown to be a promising candidate for cell transplantation in terms of biocompatibility. These strategies include the incorporation of short and extremely long G-blocks into the gelling system, in combination with varying the type and concentration of gelling ions used. The size stability of the alginate beads will be studied at physiological conditions (saline experiments). In addition, the diffusional properties of the added G-blocks will be assessed through fluorescence-labelling of the alginates, followed by confocal-laser-scanning microscopy (CLSM) analysis.



Fluorescence-labelled *L. hyperborea* leaf alginate beads, visualised by CLSM.

References

Mørch, Y. A., Donati, I., Strand, B. L. & Skjåk-Bræk, G. 2006. *Biomacromolecules,* 7**,** 1471-80.

Rokstad, A. M., Brekke, O.-L., Steinkjer, B., Ryan, L., Kollárikóva, G., Strand, B. L., Skjåk-Bræk, G., Lacík, I., Espevik, T. & Mollnes, T. E. 2011. *Acta Biomaterialia,* 7**,** 2566-2578.

Strand, B. L., Ryan, L., In't Veld, P., Kulseng, B., Rokstad, A. M., Skjåk-Bræk, G. & Espevik, T. 2001. *Cell Transplantation,* 10**,** 263-275.

Tam, S. K., Dusseault, J., Bilodeau, S., Langlois, G., Halle, J. P. & Yahia, L. 2011. *J Biomed Mater Res A,* 98**,** 40-52.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	30 sp studiepoeng / 15 studiepoeng 30 credits / 15 credits (specialization project)

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Webside / *webpage*:	
Biveileder/-e: *Co-supervisor/-s:*	**Charlotte Volpe**
Arbeidstittel på oppgaven/ *Preliminary title:*	**Evaluation of reactive oxygen species (ROS) production in microalgae**

Background and Objectives:

During the last decades there has been an increased interest in biotechnological applications of microalgae related to bioenergy and as lipid source (LC-PUFAs). In order to use these organisms for large-scale production it is essential to investigate in details how various variables influence productivity. Light is a factor of major importance as it represents the energy source of photosynthetic organisms; but too low or too high light supply will cause disadvantages in terms of growth. When present in excess, it may cause serious damages to the cells due to the formation of harmful reactive oxygen species (ROS) that leads to oxidative stress and in some cases cell death. Algae in a photobioreactor (PBR) are inevitably exposed to variation in light conditions due to mixing and natural changes in irradiation. For a cell shifting between the highly illuminated zones to the darkness, the overall photosynthetic quantum yield depends on the residence time in each zone. Once a photon is absorbed the system needs 1-15 ms to reset itself before being ready to receive another photon. If the exposure to high light conditions and the photon absorption exceed the maximum capacity of the photosystems, the reaction center can incur in over-reduction, ROS production and cell damage/death. The goal of the project is to get a better understanding of ROS production in microalgae, and to evaluate the best time intervals between light and dark to reduce ROS formation as much as possible.

Experimental methods:

The experiment will be done with one or two species of microalgae, cultured in 96 well plates. The cultures will be exposed to different light conditions carried out by a microplate light incubator. Three different light intensities will be used (three plates – high, medium, low light). For each plate, 12 different light/dark time intervals will be tested (with 8 replicates). The DCFH-DA method for ROS measurements will be used and detected with fluorescence spectrophotometric analysis. In parallel growth, autofluorescence and quantum yield analysis will be performed. The extent of the work will be adapted to the type of thesis.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, and MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	Kan tilpasses 60, 30 eller 15 studiepoeng Can be adapted to 60, 30 credits or 15 credits

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Biveileder/-e: *Co-supervisor/-s:*	**Charlotte Volpe**
Arbeidstittel på oppgaven/ *Preliminary title:*	**Random mutagenesis as a tool for strain improvement in microalgae**

Background and Objectives:

Even if the commercial potential of microalgae has been widely recognized by society, to date large scale production of microalgae for most industrial purpose (e. g. bioenergy, fish-farming, food supplement) are not yet feasible due to high production costs. For biotechnological applications like those mentioned, the phenotypical traits are critical for whether a process is profitable or not. The main strategies that can be used to maximize productivity and reduce costs of large-scale production are: Increase the lipid content per unit of biomass and increase the biomass density per culture volume or area. Strain improvement can be achieved by genetic engineering or by exposing microalgal strains to selection regime that favors certain traits. In this project the second method will be used. Random mutagenesis will be performed to increase the genetic variation in the population; afterwards those cultures will be exposed to selection regimes, which will favor certain traits.

Experimental methods:

The experiment will be performed on one or two microalgal strains. After the identification of an ideal mutagenic factor the mutagenesis will be performed on the cultures. Afterwards the cells will be exposed to two selection regime: 1) a light regime simulating the light perception of one cell in a photobioreactor that will favor cells with altered photosynthetic antennas; and 2) darkness incubation at a set point of the growth, that will favor cells with the highest lipid content. In parallel, as a control, wild type cells will be exposed to the same selection regime. Growth rate, quantum yield and autofluorescence measurement will be performed in addition to lipid analysis performed with the fluorescence method, Nile Red. The extent of the work will be adapted to the type of thesis.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	MTKJ/MIKJ, MBIOT5, and MSBIOTECH
Omfang (studiepoeng): Credits (ECTS):	Kan tilpasses 60, 30 eller 15 studiepoeng Can be adapted to 60, 30 credits or 15 credits

Hovedveileder: *Main supervisor:*	Kjell Morten Vårum
Kontaktinformasjon / epost *Contact information / email:*	kjell.m.varum@ntnu.no
Webside / *webpage*:	https://www.ntnu.no/ansatte/kjell.m.varum
Biveileder/-e: *Co-supervisor/-s:*	
Arbeidstittel på oppgaven/ *Preliminary title:*	**Molecular interactions and new gelling concepts between chitosan and fucoidan**

Kort beskrivelse av oppgaven / *Short description of the project*:

Bakgrunn og mål / *Background and Objectives:*
Fucoidan is a new and interesting polysaccharide with an interesting chemical structure and properties. Several bioactivities of fucoidan have been reported, such as anticoagulant, antithrombotic, anti-inflammatory, antiviral and immune stimulating activity. A fucoidan gel (instead of a solution) could provide beneficial properties for its applications, and the goal is to explore the experimental possibilities of preparing such gels.

Eksperimentelt / *Experimental methods:*
Chitosan-Alginate gelling systems have been studied in our group. Such gels form through ionic interactions between the positive charges on the chitosan molecules and the negative charges on the alginates, and the gelling system is controlled by changes in the pH-value. Like alginate, fucoidan also consist of negatively charged sugar units (highly sulfated fucose units), and would be expected to form gels with the positively charged chitosan through electrostatic interactions. The source for our fucoidan is the Norwegian brown seaweed *Laminaria hyperborea*. This algae is the most important raw material for production of alginate in Norway, and about 160 000 metric tons are harvested along the Norwegian coast annually, from which about 6 000 metric tons of alginate is produced. In addition to alginate, there are also other valuable components in the alga, such as fucoidan, proteins and pigments. Gelling experiments will be performed through rheological methods and Young's modulus measurements, further characterization will be performed by established methods in the biopolymer group.

Passer for (angi studie-retning/hovedprofil/-er): *Suitable for main profiles:*	Studenter med interesse for biopolymerer
Omfang (studiepoeng): Credits (ECTS):	30 sp studiepoeng / 15 studiepoeng 30 credits / 15 credits (specialization project)

Department of Biology

Hovedveileder: Main supervisor:	Henrik Jensen, Associate Professor, Centre for Biodiversity Dynamics, Department of Biology (https://www.ntnu.edu/biology/jensen-lab)
Biveileder(e): Co supervisor	Arild Husby, Thor Harald Ringsby, Bernt-Erik Sæther, and/or Jonathan Wright may be co-supervisor(s)
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Spatio-temporal dynamics of genes for ecologically important traits in house sparrows**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Knowing the genetic architecture of ecologically important traits is fundamental to our understanding of many ecological and evolutionary processes in natural populations. I can offer a number of exciting MSc-projects which focus on identifying the genetic architecture of such traits, and the causes and consequences of the traits' genetic architectures. The MSc-projects will use state-of-the-art genomic and eco-evolutionary data from a unique long-term study of a house sparrow (*Passer domesticus*) model system. Ecologically important traits are traits related to fitness (survival and reproduction) and they will therefore be important for both ecological and evolutionary dynamics in natural populations. Examples of such types of traits are morphological traits behavioural traits, physiological traits, parasite load, and life-history traits. A trait's genetic architecture consists of information on which genes affect the trait, locations of these genes in the genome, and how the genes affect the phenotype. Eco-evolutionary data have been collected on an individual based level from natural and experimental insular house sparrow populations in northern Norway since 1993. More than 27,000 individuals are included in our data base. The genomic data consists of a reference house sparrow genome, SNP-genotype data on 6500 SNPs for ca. 2300 individuals and 185,000 SNPs for ca. 4000 individuals, and information on polymorphisms within ca. 140 candidate genes for various ecologically important traits. The eco-evolutionary and genomic data will be used in statistical analyses to determine genetic architecture by mapping genes for various ecologically important traits using QTL-mapping (linkage mapping/GWAS) and/or study effects of candidate genes directly. Further statistical analyses will then be carried out to examine causes and consequences for spatio-temporal eco-evolutionary dynamics in the model system. Students choosing one of these MSc-projects will have the opportunity to get experience from fieldwork, molecular genetic laboratory work and cutting edge statistical analyses of eco-evolutionary and genomic data.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Ecology, Behaviour, Evolution and Biosystematics, Natural Resources Management, Biotechnology

Hovedveileder: Main supervisor:	Henrik Jensen, Associate Professor, Centre for Biodiversity Dynamics, Department of Biology (https://www.ntnu.edu/biology/jensen-lab)
Biveileder(e): Co supervisor	Postdoc Alina Niskanen
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**The genetic basis for inbreeding depression in house sparrows**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Anthropogenic changes of the environment, such as habitat destruction, are the major causes of high rates of population declines and extinctions. As population sizes decline they become vulnerable to inbreeding, which is expected to decrease individual fitness (called inbreeding depression) and population growth rates. As a consequence, inbreeding depression is one of the most important genetic processes affecting the persistence of small and threatened populations. Despite its importance, the genetic mechanisms underlying inbreeding depression are not well known. For example, it is unclear whether inbreeding depression is mainly caused by small genome-wide effects or single genes with large effects. We can offer MSc-projects that will focus on I) investigating the genome-wide architecture of inbreeding depression, identify specific loci important for inbreeding depression, and identify the functional genetic variation within these loci, and II) examining the interaction between environmental conditions and inbreeding depression. To achieve these goals, the projects will use state-of-the-art genomic tools, long-term individual-based data on fitness and environmental records from a unique study system of pedigreed wild house sparrow (*Passer domesticus*) populations. Data on approximately 4,000 adult house sparrows from 11 Norwegian experimental and non-experimental island populations will be used. The birds have been genotyped for 185,000 genome-wide single nucleotide polymorphisms. Students choosing one of these MSc-projects will have the opportunity to get experience from fieldwork, molecular genetic laboratory work and cutting edge statistical analyses of eco-evolutionary and genomic data.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Ecology, Behaviour, Evolution and Biosystematics, Natural Resources Management, Biotechnology

Hovedveileder: Main supervisor:	Henrik Jensen, Associate Professor, Centre for Biodiversity Dynamics, Department of Biology (https://www.ntnu.edu/biology/jensen-lab)
Biveileder(e): Co supervisor	Thor Harald Ringsby, Bernt-Erik Sæther, and/or PhD-stipendiat Dilan Saatoglu may be co-supervisor(s)
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**The genetics of dispersal in house sparrows**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Dispersal (migration) of individuals between populations may affect both ecological and evolutionary dynamics and is consequently a very important process in natural populations. For example, immigration will increase population size, reduce inbreeding and introduce genetic variation. Furthermore, dispersal reduces genetic differentiation between populations. Accurate knowledge about the number of immigrants and where they dispersed from is crucial to understand both causes and consequences of dispersal. I can offer exciting MSc-projects where the goal is to combine ecological data with genetic analyses to identify the number and origin of immigrants to natural island-populations of house sparrows (*Passer domesticus*) at the Helgeland coast in northern Norway. This information will then be used to identify population and landscape characteristics that explain variation in dispersal in space and time, and to examine the consequences of dispersal for both ecological, population genetic and evolutionary processes. Eco-evolutionary data on e.g. dispersal has been collected on an individual based level from 18 natural house sparrow populations in an island metapopulation at Helgeland since 1993. In total more than 17,500 individuals are included in this data base. The genetic data consists of genotypes on 14 microsatellites for >12000 individuals, SNP-genotype data on 6500 variable SNPs distributed across the genome for ca. 1100 individuals, and SNP-genotype data on 185,000 SNPs for ca. 3300 individuals. Students choosing one of these MSc-projects will have the opportunity to get experience from fieldwork, molecular genetic laboratory work and cutting edge statistical analyses of eco-evolutionary and genomic data.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Ecology, Behaviour, Evolution and Biosystematics, Natural Resources Management, Biotechnology

Hovedveileder: Main supervisor:	Henrik Jensen, Associate Professor, Centre for Biodiversity Dynamics, Department of Biology (https://www.ntnu.edu/biology/jensen-lab)
Biveileder(e): Co supervisor	Thor Harald Ringsby and postdoc Thomas Kvalnes
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Heritability and fitness effects of egg colour in house sparrows**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Egg colour and egg colour pattern has been shown to affect fitness in a number of bird species. This may be because colour and pattern influence the level of camouflage against predation or because colour and pattern may affect the probability of egg parasitism, either intra-specificially (e.g. by cockoo) or intra-specificially («egg dumping»). The goal of the MSc-project is to estimate the heritability (additive genetic variance) of egg colour and egg pattern, as well as genetic correlations between these traits and other fitness-related traits in house sparrows (*Passer domesticus*). Such estimates are very rare because few data sets exist where such analyses are possible. The project will then examine the effect of egg colour and pattern on individual fitness (measured by survival and reproductive output). Data on egg colour and egg pattern has been collected in up to five insular house sparrow populations at Helgeland between 2003 and 2009. Digital photographs that can be used to determine egg colour and egg pattern have been taken of more than 400 clutches. Clutches were assigned to individual females by genetic parentage analyses. Large and genetically determined pedigrees (containing almost 10,000 individuals) will be used with the data on egg colour and pattern to estimate quantitative genetic parameters using “animal models”. Students choosing this MSc-project will have the opportunity to get experience from fieldwork, molecular genetic laboratory work, quantitative genetic analyses, and statistical analyses of eco-evolutionary data.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Ecology, Behaviour, Evolution and Biosystematics, Natural Resources Management, Biotechnology

Hovedveileder: Main supervisor:	Henrik Jensen, Associate Professor, Centre for Biodiversity Dynamics, Department of Biology (https://www.ntnu.edu/biology/jensen-lab)
Biveileder(e): Co supervisor	Bernt-Erik Sæther, Thor Harald Ringsby, Henrik Pärn, and/or PhD-student Sindre Sommerli may be co-supervisor(s)
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Population genetics of water voles**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	To understand populations' ability to evolve in response to environmental change and persist in the face of habitat fragmentation and spatio-temporal fluctuations in demography due to e.g. anthropogenic effects, it is important to understand the causes and consequences of temporal changes in genetic variation within and between populations. In 2015 we started a large-scale field study on water voles (*Arvicola amphibius*) on islands at the coast of Helgeland. Our aim is that this will be a model system we can use to examine questions related to population dynamics and population genetics processes in such a fragmented system, which has large spatio-temporal fluctuations in population size. I can offer exciting MSc-projects with focus on important population genetics processes in water voles; inbreeding, genetic drift, genetic bottlenecks, founder events, and genetic population structure. Methods for genotyping individual voles on 13 microsatellites are already established. In addition, we will in collaboration with a research group at the University of Aberdeen develop high-throughput genomic resources for water voles that we aim to use in the proposed MSc-projects. Students choosing these MSc-projects will gain skills in carrying out high-quality fieldwork on the beautiful Helgeland coast, experience with molecular genetic laboratory work, and good knowledge about statistical analyses of population genetic data.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Ecology, Behaviour, Evolution and Biosystematics, Natural Resources Management, Biotechnology

Hovedveileder: Main supervisor:	Jens Rohloff
Biveileder(e): Co supervisor	Richard Strimbeck
Arbeidstittel på oppgaven (max 20 word): Preliminary title:	**Ecological Urban Production of Vegetables**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	The master project(s) is/are integrated as part of a regional research project aiming at the utilisation of compost derived from manure and food waste for the ecological production of vegetables. Major active partners involve Skjetlein vgs (*Naturbrukslinje*) and the company Global Green Energy (GGE). Sub-goals include (a) Development and optimisation of compost products (mixtures) to be used as growth substrate (b) Increase knowledge about innovative soil substrate(s) by the use of a compost bioreactor (c) Improve recruitment to education and research within urban farming and ecological food production Possible master projects: 1. Investigation of effects of compost products in vegetable production (e.g. tomato, salad, herbs) on crop growth, yield and quality. Focus areas: plant physiology, phytochemistry, food chemistry 2. Investigation of effects of manure/food waste ratio and bioreactor conditions on composting process and composition with regard to soil substrate quality and commercial value. Focus areas: microbiology, biochemistry, agriculture
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Biology, Biotechnology, LUR

Hovedveileder: Main supervisor:	Thorsten Hamann
Biveileder(e): Co supervisor	Timo Engelsdorf
Arbeidstittel på oppgaven (max 20 word): Preliminary title:	**Functional analysis of candidate genes mediating plant cell wall integrity maintenance**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	The plant cell wall is the first line of defense of all plants against stress. It is a highly dynamic structure, which also provides different materials relevant for society. Plant cell wall signaling processes are essential during defense and are also intricately involved in maintaining functional integrity of the cell wall during growth and response to biotic stress. Recently the host lab has performed extensive transcriptomics and phospho-proteomics experiments to identify genes maintaining plant cell wall integrity during development and defense in *Arabidopsis thaliana*. The aim of the project is to functionally characterize several of these candidate genes in order to dissect the molecular mechanism underlying plant cell wall integrity maintenance. The project will initially involve sterile tissue culture work to generate biological material, qRT-PCR-based confirmation of transcriptomics results, LC-MS-based measurements of phytohormones in gene knockout plants, cloning of reporter-protein fusion and promoter reporter constructs, which will be followed by generation of transgenic plants to perform cellbiological and expression studies using advanced microscopy (confocal microscopy in combination with image analysis). Generating the data on gene function is the prerequisite to achieve the long-term of this project, which is to use the genes identified in Arabidopsis as leads to improve performance of food crops and facilitate bioenergy production from ligno-cellulosic biomass.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Biologi, bioteknologi

Hovedveileder: Main supervisor:	Thorsten Hamann
Biveileder(e): Co supervisor	Timo Engelsdorf
Arbeidstittel på oppgaven (max 20 word): Preliminary title:	**Development of novel analytical tools to analyze plant cell wall signaling**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Plant cell wall signaling processes are essential during interaction between the plant and the environment as well as during development. They are also intricately involved in maintaining functional integrity of the cell wall during growth and response to biotic stress. Currently there are no suitable tools available to study early, fast cell biological processes during cell wall integrity maintenance. The host lab has performed recently extensive transcriptomics experiments and identified genes, which are responding to cell wall integrity impairment. The aim of the project is to use the candidate genes as starting place to develop novel markers. The project will initially involve tissue culture work to generate biological material, qRT-PCR-based confirmation of transcriptomics results and cloning of reporter-protein fusion constructs, which will be followed by generation of transgenic plants to perform cellbiological studies of the reporter fusion constructs using advanced microscopy (confocal microscopy in combination with image analysis).
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Biologi, bioteknologi

Hovedveileder: Main supervisor:	Professor Berit Johansen
Biveileder(e): Co supervisor	Dr. Astrid Feuerherm, Dr Thuy Nguyen, Dr. Linn-Karina Selvik
Arbeidstittel på oppgaven (max 20 word): Preliminary tittel:	**Lipid signaling mechanisms in inflammation.**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Obesity is a major risk factor for lifestyle diseases. Lifestyle is affecting severity of chronic diseases, including cardiovascular diseases and rheumatism. Common symptom between obesity, lifestyle and chronic disease is inflammation (1,2). Investigations regarding molecular mechanisms of inflammation will give insights on how different aspects of lifestyle, hormonal responses, e.g. insulin, will affect disease progression and severity (3,4). Hormones under study include cytokines, insulin, chemokines, eicosanoids and adipokines. Model systems: Synoviocytes, cellular model for rheumatoid arthritis; Monocytes, cellular model for white blood cells. Possible master theses: 1) Characterization of insulin signaling in synoviocytes 2) Characterization of adipokin signaling in synoviocytes 3) Characterization of microRNA as a regulatory mechanism of synoviocyte biology 4) Characterisation of TLR2/4-induced responses, and possible involvement of cPLA2 in an osteoclast cell model 5) Metabolomics detection human samples (collaboration with Dr Jens Rohloff) 6) Systems biology of human intervention samples (collaboration with Prof. Martin Kuiper.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	MBIOT5, MBI-celle/molekylærbiologi, MSc Biotechnology (2yr)

1. WHO, *Global status report on noncommunicable diseases 2010. Description of the global burden of NCDs, their risk factors and determinants.*, WHO, Editor. 2011. p. 1-176.

2. Kelly, T., et al., *Global burden of obesity in 2005 and projections to 2030.* International Journal of Obesity, 2008. 32(9): p. 1431-1437.

3. Ouchi, N., et al., *Adipokines in inflammation and metabolic disease.* Nat Rev Immunol. 11(2): p. 85-97.

4. Gregor, M.F. and G.S. Hotamisligil, *Inflammatory mechanisms in obesity.* Annu Rev Immunol, 2011. 29: p. 415-45.

Hovedveileder: Main supervisor:	Martin Kuiper - kuiper@ntnu.no – 73550348 – DU1-111 IBI
Biveileder(e): Co supervisor	Astrid Lagreid, IKM-DMF; several other co-supervisors (IBI, IBT) are possible, depending on the design of the master proposal.
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Implementation of Boolean models for cell perturbation analysis and drug development**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	The use of network and model based approaches to describe, explain and understand biological processes is an essential approach in Systems Biology. Tools that enable this approach range from Cytoscape (network based) to CellDesigner (pathway-based) to full-fledged mathematical modeling platforms. One of the more basic modeling paradigms is based on Boolean logics, where interactions between model components (proteins, genes) only need to be described in terms of activation and inhibition, and the regulatory rules are described using AND, OR, and NOT logics. We are developing user-friendly, semi-automated software tools (see Flobak et al 2015), in the new initiative DrugLogics (www.DrugLogics-NTNU.org), part of the NTNU Digital Life theme. DrugLogics aims to develop Boolean model based approaches to help develop Personalized Medicine approaches to treat cancer. This initiative offers possibilities for a variety of Master projects: - The assembly of a ‘causal statement’ knowledge base that integrates information from resources like Reactome and SIGNOR that can be used to build Boolean models - The use of our curation tool SciCura to convert information from literature in the form of causal statements to the knowledge base - The building of Boolean models to simulate the effect of experimental perturbations on the behavior of specific cells (plant, animal, microorganism) - The simulation of these Boolean models to predict the effects of mutations or other perturbations and the subsequent experimental validation - and many more …
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Biology / Biotechnology
Reference:	Flobak Å et al. Discovery of drug synergies in gastric cancer cells predicted by logical modelling. PloS Comp. Biol. 2015 DOI: 10.1371/journal.pcbi.1004426. www.druglogics-ntnu.org www.colosys.org https://www.ntnu.edu/crossover-research https://www.ntnu.edu/health/druglogics www.reactome.org, http://signor.uniroma2.it/

Hovedveileder: Main supervisor:	Augustine Arukwe
Biveileder(e): Co supervisor	
Arbeidstittel på oppgaven (max 20 word): Preliminary titel:	**Identification of key cellular targets of toxicants as potential *xenosensor* biomolecules in fish**
Kort beskrivelse av oppgaven (max 300 word): Short description of the project:	Our group is part of a big NFR funded biotechnology "Digital life" project entitled "dCod 1.0: decoding systems toxicology of Atlantic cod (*Gadus morhua*) – environmental genomics for ecosystem quality monitoring and risk assessment" in collaboration with several national (UiB, UiO, NMBU) and international partners The project will pursue a research line in environmental omics that identifies key cellular targets of toxicants as potential *xenosensor* biomolecules. An illustrating example is the use of transcription factors such as the peroxisome proliferator-activated receptors (PPARs), aryl hydrocarbon receptor (AhR) and estrogen receptor (ER) in multiple assays for toxicants and endocrine disruptors in fish systems. We are looking for 4-5 master students to work together with a PhD fellow in delivering our part of the project. We will develop and structure out a candidate-specific *in vivo* or *in vitro* research plan that fits with the overall aims of dCod. Otherwise, the overall objective of our research is to develop diagnostic gene, enzyme and protein response tools in the study of the molecular and physiological mechanisms of the effects of xenoestrogens and xenobiotic, and their interactions in wildlife species. In our laboratory, these studies are performed in both *in vitro* and *in vivo* systems.
Oppgaven passer for (angi studieretning(er)): Suitable for (main profiles):	Environmental Toxicology and Chemistry; cell and molecular biology